

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/553,661

CRF Edit Date: 11/1/05
Edited by: [Signature]

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

___ Deleted ☒ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

___ Other:



PCT

RAW SEQUENCE LISTING

DATE: 11/01/2005

PATENT APPLICATION: US/10/553,661

TIME: 11:57:18

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\11012005\J553661.raw

3 <110> APPLICANT: Genesis Group Inc., Kenneth Kao, Catherine Popadiuk
 5 <120> TITLE OF INVENTION: Pygopus in Diagnosis and Treatment of Cancer
 7 <130> FILE REFERENCE: 50680-4
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/553,661
 C--> 9 <141> CURRENT FILING DATE: 2005-10-17
 9 <150> PRIOR APPLICATION NUMBER: US 60/463 309
 10 <151> PRIOR FILING DATE: 2003-04-17
 12 <150> PRIOR APPLICATION NUMBER: US 60/496 012
 13 <151> PRIOR FILING DATE: 2003-08-19
 15 <160> NUMBER OF SEQ ID NOS: 28
 17 <170> SOFTWARE: PatentIn version 3.3
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 3190
 21 <212> TYPE: DNA
 22 <213> ORGANISM: homosapiens
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: hPygo-2
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (173)..(1393)
 31 <400> SEQUENCE: 1
 32 gtctggagag agcgcgcagt ttgcgcggcg gctcggcgct tccctgtcgt cgcactttgt 60
 34 ggttgcgtgca gctcgggggc ctgggctgcc cctgacaccc cttctgggcg atggtgcagc 120
 36 ccaagggcgc ctccatcccc cgccgctgcc gctaaccggc gtccccact cc atg gcc 178
 37 Met Ala
 38 1
 40 gcc tcg gcg ccg ccc cca ccg gac aag ctg gag gga ggt ggc ggc ccc 226
 41 Ala Ser Ala Pro Pro Pro Pro Asp Lys Leu Glu Gly Gly Gly Gly Pro
 42 5 10 15
 44 gca ccg ccc cct gcg ccg ccc agc acc ggg agg aag cag ggc aag gcc 274
 45 Ala Pro Pro Pro Ala Pro Pro Ser Thr Gly Arg Lys Gln Gly Lys Ala
 46 20 25 30
 48 ggt ctg caa atg aag agt cca gaa aag aag cga agg aag tca aat act 322
 49 Gly Leu Gln Met Lys Ser Pro Glu Lys Lys Arg Arg Lys Ser Asn Thr
 50 35 40 45 50
 52 cag ggc cct gca tac tca cat ctg acg gag ttt gca cca ccc cca act 370
 53 Gln Gly Pro Ala Tyr Ser His Leu Thr Glu Phe Ala Pro Pro Pro Thr
 54 55 60 65
 57 ccc atg gtg gat cac ctg gtt gca tcc aac cct ttt gaa gat gac ttc 418
 58 Pro Met Val Asp His Leu Val Ala Ser Asn Pro Phe Glu Asp Asp Phe
 59 70 75 80
 61 gga gcc ccc aaa gtg ggg gtt gca gcc cct cca ttc ctt ggc agt cct 466
 62 Gly Ala Pro Lys Val Gly Val Ala Ala Pro Pro Phe Leu Gly Ser Pro

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63	85	90	95	
65	gtg ccc ttc gga ggc ttc cgt	gtg cag ggg ggc atg gcg ggc cag gta	514	
66	Val Pro Phe Gly Gly Phe Arg	Val Gln Gly Gly Met Ala Gly Gln Val		
67	100	105	110	
69	ccc cca ggc tac agc act gga ggt gga ggg ggc	ccc cag cca ctc cgt	562	
70	Pro Pro Gly Tyr Ser Thr Gly Gly Gly Gly Gly	Pro Gln Pro Leu Arg		
71	115	120	125	130
73	cga cag cca ccc ccc ttc cct ccc aat cct atg ggc	cct gct ttc aac	610	
74	Arg Gln Pro Pro Pro Phe Pro Pro Asn Pro Met Gly	Pro Ala Phe Asn		
75	135	140	145	
77	atg ccc ccc cag ggt cct ggc tac cca ccc cca ggc	aac atg aac ttt	658	
78	Met Pro Pro Gln Gly Pro Gly Tyr Pro Pro Pro Gly	Asn Met Asn Phe		
79	150	155	160	
81	ccc agc caa ccc ttc aac cag cct ctg ggt caa aac	ttt agt cct ccc	706	
82	Pro Ser Gln Pro Phe Asn Gln Pro Leu Gly Gln Asn	Phe Ser Pro Pro		
83	165	170	175	
85	agt ggg cag atg atg ccg ggc cca gtg ggg gga ttt	ggt ccc atg atc	754	
86	Ser Gly Gln Met Met Pro Gly Pro Val Gly Gly Phe	Gly Pro Met Ile		
87	180	185	190	
89	tca ccc acc atg gga cag cct ccc aga gca gag ctg	ggc cca cct tct	802	
90	Ser Pro Thr Met Gly Gln Pro Pro Arg Ala Glu	Leu Gly Pro Pro Ser		
91	195	200	205	210
93	ctg tcc caa cga ttt gct cag cca ggg gct cct ttt	ggc cct tct cct	850	
94	Leu Ser Gln Arg Phe Ala Gln Pro Gly Ala Pro Phe	Gly Pro Ser Pro		
95	215	220	225	
97	ctc cag aga cct ggt cag ggg ctc ccc agc ctg ccg	cct aac aca agt	898	
98	Leu Gln Arg Pro Gly Gln Gly Leu Pro Ser Leu Pro	Pro Asn Thr Ser		
99	230	235	240	
101	ccc ttt cct ggt ccg gac cct ggc ttt cct ggc	cct ggt ggt gag gat	946	
102	Pro Phe Pro Gly Pro Asp Pro Gly Phe Pro Gly	Pro Gly Gly Glu Asp		
103	245	250	255	
105	ggg ggg aag ccc ttg aat cca cct gct tct act gct	ttt ccc cag gag	994	
106	Gly Gly Lys Pro Leu Asn Pro Pro Ala Ser Thr	Ala Phe Pro Gln Glu		
107	260	265	270	
109	ccc cac tca ggc tcc ccg gct gct gct gtt aat ggg	aac cag ccc agt	1042	
110	Pro His Ser Gly Ser Pro Ala Ala Ala Val Asn	Gly Asn Gln Pro Ser		
111	275	280	285	290
114	ttc ccc ccg aac agc agt ggg ccg ggt ggg ggc	act cca gat gcc aac	1090	
115	Phe Pro Pro Asn Ser Ser Gly Arg Gly Gly Gly	Thr Pro Asp Ala Asn		
116	295	300	305	
118	agc ttg gca ccc cct ggc aag gca ggt ggg ggc	tcc ggg ccc cag cct	1138	
119	Ser Leu Ala Pro Pro Gly Lys Ala Gly Gly Gly	Ser Gly Pro Gln Pro		
120	310	315	320	
122	ccc cca ggc ttg gtg tac cca tgt ggt gcc tgt	ccg agt gag gtg aac	1186	
123	Pro Pro Gly Leu Val Tyr Pro Cys Gly Ala Cys	Arg Ser Glu Val Asn		
124	325	330	335	
126	gat gac cag gat gcc att ctg tgt gag gcc tcc	tgc cag aaa tgg ttc	1234	
127	Asp Asp Gln Asp Ala Ile Leu Cys Glu Ala Ser	Cys Gln Lys Trp Phe		
128	340	345	350	

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DATE: 11/01/2005

TIME: 11:57:18

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130 cac cgt gag tgc aca ggc atg act gag agc gcc tat ggg ctg ctg acc      1282
131 His Arg Glu Cys Thr Gly Met Thr Glu Ser Ala Tyr Gly Leu Leu Thr
132 355                               360                               365                               370
134 act gaa gct tct gcc gtc tgg gcc tgc gat ctc tgc ctc aag acc aag      1330
135 Thr Glu Ala Ser Ala Val Trp Ala Cys Asp Leu Cys Leu Lys Thr Lys
136                               375                               380                               385
138 gag atc cag tct gtc tac atc cgt gag ggc atg ggg cag ctg gtg gct      1378
139 Glu Ile Gln Ser Val Tyr Ile Arg Glu Gly Met Gly Gln Leu Val Ala
140                               390                               395                               400
142 gct aac gat ggg tga cgctgggtgaa gtggcccagg gaagtgcaca tgtctctccc      1433
143 Ala Asn Asp Gly
144                               405
146 tgctcttcca ggggtgatttt tttgatgttt ggctcttggt ccttgtttcc actggctttc      1493
147 catcccatg gggcagaaac agtggctcct gggagcagaa aaggaattga ggtgggcagg      1553
148 cagaagagcc tggattgtct actgttttgg gaaacttaca tgttgagatc tacagagatc      1613
149 caggaaacca aagccctgct gagcagagcc attttgtggc tatttctgga ggcccaggag      1673
150 tgtggctgca agagaaaagg ggctggagga agatccggag ggcaggggtg ttcctctgctc      1733
151 tgatgatgga tgcccctaac acctgtgcct aacacccta ctgaaccca cagctccagc      1793
152 cttagttttt ggagtcaagt gttaaagggt tctggccaga ggaattgggg tcttgccatc      1853
153 cctgcaatag cccttttatg ggctctggga gacagcttta ggaataaat ggggattttc      1913
154 ccctttttct acccactcct ttgcttcctc caagacttac ccaactcctt cccctcaga      1973
155 gaaccaaata gcctgaggaa gcaggagagt tcttggttat ggcagtttct tgggtatttg      2033
156 gggcttcaag acagtaggtg agagatgctg tcaggacgta tcttcttcat accaaagtca      2093
157 ctggctcttt ctacgctct ctctgtcttt tctcctaata accatatttt tgccaaaaat      2153
158 tgggatattg tatctgacag accagaatat ttgaagtttg ggctgtcctg aaagtctgga      2213
159 ctttgggtgg accctcctcc ccagcccat ctgttgacaa ttatactccg tgtgttcttc      2273
160 aactttcggc gcccttatcc ccctgccttc ctggcttgat tgaaggaaag cttgaaaagg      2333
161 cgcagagccc tatacctcat ttcctccatg ataaaaggat ccaagtgagg ccctgtcaca      2393
162 gcctgtgggt aggggatgag gggggatcct cattgccatg gtactcaaag gtagaagagc      2453
163 ctggagtttg ttgcttctct ttgctattct ttcatactct cttgggcctg gtgattaatt      2513
164 agcaattctc attcctctca gccaaaggcc tgcactgggc tttatttgtc tttttttatt      2573
165 ttttaagcac tgcttgccag agatgggcct ggggcctgat gaggacctta gcgctgctcg      2633
166 ttctcctttt ctgttcatgc acacattcct ccatgggggt ggggaaggcag gcatgggggtg      2693
167 tggccctcgg agaagttagg agtccccag ctcaagatac agtggcaaag acctagtgg      2753
168 cccctacccc cacttctctc agttcctggc atgaggagag aagaccctgc tctgggtggag      2813
169 ctgacaacct ttgaggctgg gaggagagca gcctctgggc atcgttccca gtgtccctca      2873
170 cactaaaacg gcgtagatgg caacccccca cccccaccc gctgctcaac tcttgtgttt      2933
171 gttgttctgt ttgccccatt tatctgttgc tgtttttgtg ttgtcttccc ctgctccgca      2993
172 ttttgtaaaa tggcccttgg gggagtggtt ttgctggatc tgctccctct cgctctctca      3053
173 ctccactact ttttgacaaa agtgatggca gaatgcggtg gtgggtgggg tcttttgtac      3113
174 tgttgatta ataaaatgat tttaaaatcc caaaaaaaaa aaaaaaaaaa aaaaaaaaaa      3173
175 aaaaaaaaaa aaaaaaa
176                               3190
178 <210> SEQ ID NO: 2
179 <211> LENGTH: 406
180 <212> TYPE: PRT
181 <213> ORGANISM: homosapiens
183 <220> FEATURE:
184 <223> OTHER INFORMATION: hPygo-2
186 <400> SEQUENCE: 2

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RAW SEQUENCE LISTING

DATE: 11/01/2005

PATENT APPLICATION: US/10/553,661

TIME: 11:57:18

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\11012005\J553661.raw

```

188 Met Ala Ala Ser Ala Pro Pro Pro Pro Asp Lys Leu Glu Gly Gly Gly
189 1 5 10 15
191 Gly Pro Ala Pro Pro Pro Ala Pro Pro Ser Thr Gly Arg Lys Gln Gly
192 20 25 30
194 Lys Ala Gly Leu Gln Met Lys Ser Pro Glu Lys Lys Arg Arg Lys Ser
195 35 40 45
197 Asn Thr Gln Gly Pro Ala Tyr Ser His Leu Thr Glu Phe Ala Pro Pro
198 50 55 60
200 Pro Thr Pro Met Val Asp His Leu Val Ala Ser Asn Pro Phe Glu Asp
201 65 70 75 80
203 Asp Phe Gly Ala Pro Lys Val Gly Val Ala Ala Pro Pro Phe Leu Gly
204 85 90 95
206 Ser Pro Val Pro Phe Gly Gly Phe Arg Val Gln Gly Gly Met Ala Gly
207 100 105 110
209 Gln Val Pro Pro Gly Tyr Ser Thr Gly Gly Gly Gly Gly Pro Gln Pro
210 115 120 125
212 Leu Arg Arg Gln Pro Pro Pro Phe Pro Pro Asn Pro Met Gly Pro Ala
213 130 135 140
215 Phe Asn Met Pro Pro Gln Gly Pro Gly Tyr Pro Pro Pro Gly Asn Met
216 145 150 155 160
218 Asn Phe Pro Ser Gln Pro Phe Asn Gln Pro Leu Gly Gln Asn Phe Ser
219 165 170 175
221 Pro Pro Ser Gly Gln Met Met Pro Gly Pro Val Gly Gly Phe Gly Pro
222 180 185 190
224 Met Ile Ser Pro Thr Met Gly Gln Pro Pro Arg Ala Glu Leu Gly Pro
225 195 200 205
228 Pro Ser Leu Ser Gln Arg Phe Ala Gln Pro Gly Ala Pro Phe Gly Pro
229 210 215 220
231 Ser Pro Leu Gln Arg Pro Gly Gln Gly Leu Pro Ser Leu Pro Pro Asn
232 225 230 235 240
234 Thr Ser Pro Phe Pro Gly Pro Asp Pro Gly Phe Pro Gly Pro Gly Gly
235 245 250 255
237 Glu Asp Gly Gly Lys Pro Leu Asn Pro Pro Ala Ser Thr Ala Phe Pro
238 260 265 270
240 Gln Glu Pro His Ser Gly Ser Pro Ala Ala Ala Val Asn Gly Asn Gln
241 275 280 285
243 Pro Ser Phe Pro Pro Asn Ser Ser Gly Arg Gly Gly Gly Thr Pro Asp
244 290 295 300
246 Ala Asn Ser Leu Ala Pro Pro Gly Lys Ala Gly Gly Gly Ser Gly Pro
247 305 310 315 320
249 Gln Pro Pro Pro Gly Leu Val Tyr Pro Cys Gly Ala Cys Arg Ser Glu
250 325 330 335
252 Val Asn Asp Asp Gln Asp Ala Ile Leu Cys Glu Ala Ser Cys Gln Lys
253 340 345 350
255 Trp Phe His Arg Glu Cys Thr Gly Met Thr Glu Ser Ala Tyr Gly Leu
256 355 360 365
258 Leu Thr Thr Glu Ala Ser Ala Val Trp Ala Cys Asp Leu Cys Leu Lys
259 370 375 380
261 Thr Lys Glu Ile Gln Ser Val Tyr Ile Arg Glu Gly Met Gly Gln Leu

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TIME: 11:57:18

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\11012005\J553661.raw

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262 385          390          395          400
264 Val Ala Ala Asn Asp Gly
265          405
268 <210> SEQ ID NO: 3
269 <211> LENGTH: 1260
270 <212> TYPE: DNA
271 <213> ORGANISM: homosapiens
273 <220> FEATURE:
274 <221> NAME/KEY: CDS
275 <222> LOCATION: (1)..(1260)
277 <220> FEATURE:
278 <223> OTHER INFORMATION: hPygo-1
280 <400> SEQUENCE: 3
281 atg ccc gcc gag aac tct cca gct ccc gct tac aaa gtt tcc tcg cat      48
282 Met Pro Ala Glu Asn Ser Pro Ala Pro Ala Tyr Lys Val Ser Ser His
283 1          5          10          15
285 ggt ggt gat agt gga ctg gat ggg tta gga gga cca ggt gta caa cta      96
286 Gly Gly Asp Ser Gly Leu Asp Gly Leu Gly Gly Pro Gly Val Gln Leu
287          20          25          30
289 gga agc cca gat aag aaa aag cgc aag gca aat aca cag gga cct tct      144
290 Gly Ser Pro Asp Lys Lys Lys Arg Lys Ala Asn Thr Gln Gly Pro Ser
291          35          40          45
293 ttc cct cca ttg tct gag tat gct cca cca ccg aat cca aac tct gac      192
294 Phe Pro Pro Leu Ser Glu Tyr Ala Pro Pro Pro Asn Pro Asn Ser Asp
295          50          55          60
297 cat cta gtg gct gct aat cca ttt gat gac aac tat aat act att tcc      240
298 His Leu Val Ala Ala Asn Pro Phe Asp Asp Asn Tyr Asn Thr Ile Ser
299 65          70          75          80
301 tat aaa cca cta cct tcg tca aat cca tat ctt ggc cct ggt tat cct      288
302 Tyr Lys Pro Leu Pro Ser Ser Asn Pro Tyr Leu Gly Pro Gly Tyr Pro
303          85          90          95
305 ggc ttt gga ggc tat agt aca ttc aga atg cca cct cac gtt ccc cca      336
306 Gly Phe Gly Gly Tyr Ser Thr Phe Arg Met Pro Pro His Val Pro Pro
307          100         105         110
309 aga atg tct tcc cca tac tgt ggt cct tac tca ctc agg aac cag cca      384
310 Arg Met Ser Ser Pro Tyr Cys Gly Pro Tyr Ser Leu Arg Asn Gln Pro
311          115         120         125
313 cac cca ttt cct cag aat cct ctg ggc atg ggt ttt aat cga cct cat      432
314 His Pro Phe Pro Gln Asn Pro Leu Gly Met Gly Phe Asn Arg Pro His
315          130         135         140
317 gct ttt aac ttt ggg cca cat gat aat tca agt ttc ggt aat cca tct      480
318 Ala Phe Asn Phe Gly Pro His Asp Asn Ser Ser Phe Gly Asn Pro Ser
319 145          150         155         160
321 tat aat aat gca cta agt cag aat gtc aac atg cct aat caa cat ttt      528
322 Tyr Asn Asn Ala Leu Ser Gln Asn Val Asn Met Pro Asn Gln His Phe
323          165         170         175
325 aga caa aat cct gct gaa aat ttc agt caa att cct cca cag aat gct      576
326 Arg Gln Asn Pro Ala Glu Asn Phe Ser Gln Ile Pro Pro Gln Asn Ala
327          180         185         190

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/553,661

DATE: 11/01/2005
TIME: 11:57:19

Input Set : A:\PTO.AMC.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28

VERIFICATION SUMMARY

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Input Set : A:\PTO.AMC.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date